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General information about the entry

Entry name **SP3E_BACSU**
 Primary accession number **P21458**
 Secondary accession number P21459
 Entered in SWISS-PROT in Release 18, May 1991
 Sequence was last modified in Release 31, February 1995
 Annotations were last modified in Release 41, June 2002

Name and origin of the protein

Protein name **Stage III sporulation protein E**
 Synonyms None
 Gene name **SPOIIE**
 From Bacillus subtilis [TaxID: 1423]
 Taxonomy Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=168;
 MEDLINE=88199510; PubMed=3129532; [NCBI, ExPASy, EBI, Israel, Japan]
 Butler P.D., Mandelstam J.;
 "Nucleotide sequence of the sporulation operon, spoIIIE, of *Bacillus subtilis*."; *J. Gen. Microbiol.* 133:2359-2370(1987).

[2] REVISIONS.

MEDLINE=90014185; PubMed=2507870; [NCBI, ExPASy, EBI, Israel, Japan]
 Foulger D., Errington J.;
 "The role of the sporulation gene spoIIIE in the regulation of prespore-specific gene expression in *Bacillus subtilis*."; *Mol. Microbiol.* 3:1247-1255(1989).

[3] SEQUENCE FROM NUCLEIC ACID.

STRAIN=168;
 MEDLINE=98044033; PubMed=9384377; [NCBI, ExPASy, EBI, Israel, Japan]
 Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D.,

Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.
 "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*."; *Nature* 390:249-256(1997).

[4] CHARACTERIZATION.

MEDLINE=94212172; PubMed=8160014; [NCBI, ExPASy, EBI, Israel, Japan]

Wu L.J., Errington J.;

"*Bacillus subtilis* spoIIIE protein required for DNA segregation during asymmetric cell division."; *Science* 264:572-575(1994).

Comments

- **FUNCTION:** REQUIRED FOR SPORULATION. IT IS REQUIRED FOR CHROMOSOME SEGREGATION INTO THE PRESPORE COMPARTMENT. MAY ALSO BE REQUIRED TO PREVENT SIGMA F FROM BECOMING ACTIVE IN THE MOTHER CELL. MAY BIND DNA.
- **SUBCELLULAR LOCATION:** Integral membrane protein (*Potential*).
- **SIMILARITY:** BELONGS TO THE FTSK/SPOIIIE FAMILY.

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Cross-references

EMBL	M17445; AAA22784.1; ALT_SEQ.[EMBL / GenBank / DDBJ] [CoDingSequence] M17445; AAA22785.1; ALT_SEQ.[EMBL / GenBank / DDBJ] [CoDingSequence] Z99112; CAB13553.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A32269; A32269. B32269; B32269. S09411; S09411.
SubtiList	BG10763; spoIIIE. [SubtiList / NRSUB / Micado]
InterPro	IPR002543; FtsK_SpoIIIE. Graphical view of domain structure.
Pfam	PF01580; FtsK_SpoIIIE; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	P21458 .
ProtoNet	P21458 .

ProtoMap [P21458](#).
 PRESAGE [P21458](#).
 DIP [P21458](#).
 ModBase [P21458](#).
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Keywords

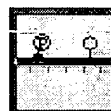
Sporulation; ATP-binding; Transmembrane; Complete proteome.

Features

Key	From	To	Length	Description
TRANSMEM	22	42	21	POTENTIAL.
TRANSMEM	52	72	21	POTENTIAL.
TRANSMEM	87	107	21	POTENTIAL.
TRANSMEM	154	174	21	POTENTIAL.
NP_BIND	467	474	8	ATP (POTENTIAL).



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Sequence information

Length: **787** Molecular weight: **87153** CRC64: **316F40F6112816E3** [This is a checksum on the sequence]

10	20	30	40	50	60
MAKKKRKSRK	KQAKQLNIKY	ELNGLLCIAI	SIIAILQLGV	VGQTFIYLF	RFAGEWFLC
70	80	90	100	110	120
LLGLLVLGVS	LFWKKTTPSL	LTRRKAGLYC	IIASILLLSH	VQLFKNLTHK	GSIESASVVR
130	140	150	160	170	180
NTWELFLMDM	NGSSASPDLG	GGMIGALLFA	ASHFLFASTG	SQIMAIVMIL	IGMILVTGRS
190	200	210	220	230	240
LQETLKKWMS	PIGRFIKEQW	LAFIDDMKSF	KSNMQSSKKT	KAPSKKQKPA	RKKQQMEPEP
250	260	270	280	290	300
PDEEGDYETV	SPLIHSEPII	SSFSDRNEEE	ESPVIEKRAE	PVSKPLQDIQ	PETGDQETVS
310	320	330	340	350	360
APPMFTFELE	NKDYEMPSLD	LLADPKHTGQ	QADKKNIYEN	ARKLERTFQS	FGVKAKVTQV
370	380	390	400	410	420
HLGPAVTKEY	VYPDVGKVS	KIVNLSDDLA	LALAAKDIRI	EAPIPGKSAI	GIEVPNAEVA
430	440	450	460	470	480
MVSLKEVLES	KLNDRPDANV	LIGLGRNISG	EAVLAELNKM	PHLLVAGATG	SGKSVCVNGI
490	500	510	520	530	540

```

ITSILMRAKP HEVKMMIDP KMVELNVYNG IPHLLAPVVT DPKKASQALK KVVNEMERRY
      550      560      570      580      590      600
      |      |      |      |      |      |
ELFSHTGTRN IEGYNDYIKR ANNEEGAKQP ELPYIVVIVD ELADLMMVAS SDVEDSITRL
      610      620      630      640      650      660
      |      |      |      |      |      |
SQMARAAGIH LIIATQRPSV DVITGVIKAN IPSRIAFSVS SQTDSRTILD MGGAEKLLGR
      670      680      690      700      710      720
      |      |      |      |      |      |
GDMLFLPVGA NKPVRVQGAF LSDDEVEKVV DHVITQKKAQ YQEEMIP EET TETHSEVTDE
      730      740      750      760      770      780
      |      |      |      |      |      |
LYDEAVELIV GMQTASVSML QRRFRIGYTR AARLIDAMEE RGVVGPYEGS KPREVLLSKE

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General information about the entry

Entry name **FTSI_ECOLI**
 Primary accession number **P04286**
 Secondary accession numbers None
 Entered in SWISS-PROT in Release 04, March 1987
 Sequence was last modified in Release 04, March 1987
 Annotations were last modified in Release 41, June 2002
 Name and origin of the protein
 Protein name **Peptidoglycan synthetase ftsI [Precursor]**
 Synonyms **Penicillin-binding protein 3**
PBP-3
 Gene name **FTSI or PBPB or B0084 or Z0094 or ECS0088**
 From Escherichia coli [TaxID: 562]
Escherichia coli O157:H7 [TaxID: 83334]
 Taxonomy Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=K12;
 MEDLINE=83296957; PubMed=6350821; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Nakamura M., Maruyama I.N., Soma M., Kato J., Suzuki H., Horota Y.;
 "On the process of cellular division in Escherichia coli: nucleotide sequence of the gene for penicillin-binding protein 3.";
 Mol. Gen. Genet. 191:1-9(1983).
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=K12;
 MEDLINE=92334977; PubMed=1630901; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.;
 "Systematic sequencing of the Escherichia coli genome: analysis of the 0-2.4 min region.";
 Nucleic Acids Res. 20:3305-3308(1992).
- [3] SEQUENCE FROM NUCLEIC ACID.
STRAIN=K12 / MG1655;
 MEDLINE=97426617; PubMed=9278503; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of *Escherichia coli* K-12.";
Science 277:1453-1474(1997).

[4] SEQUENCE FROM NUCLEIC ACID.

STRAIN=O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; **PubMed**=11206551; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
Nature 409:529-533(2001).

[5] SEQUENCE FROM NUCLEIC ACID.

STRAIN=O157:H7 / RIMD 0509952;
MEDLINE=21156231; **PubMed**=11258796; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).

[6] SEQUENCE OF 1-71 FROM NUCLEIC ACID.

MEDLINE=93077472; **PubMed**=1447153; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Ueki M., Wachi M., Jung H.K., Ishino F., Matsubashi M.;
"Escherichia coli *mraR* gene involved in cell growth and division.";
J. Bacteriol. 174:7841-7843(1992).

[7] SEQUENCE OF 1-41 FROM NUCLEIC ACID.

MEDLINE=93077455; **PubMed**=1332942; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Guzman L.M., Barondess J.J., Beckwith J.;
"FtsL, an essential cytoplasmic membrane protein involved in cell division in *Escherichia coli*.";
J. Bacteriol. 174:7716-7728(1992).

[8] SEQUENCE OF 550-588 FROM NUCLEIC ACID.

MEDLINE=90328986; **PubMed**=2198024; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Michaud C., Parquet C., Flouret B., Blanot D., van Heijenoort J.;
"Revised interpretation of the sequence containing the *murE* gene encoding the UDP-N-acetylmuramyl-tripeptide synthetase of *Escherichia coli*.";
Biochem. J. 269:277-280(1990).

[9] MUTAGENESIS OF SER-307.

MEDLINE=86117937; **PubMed**=3911028; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Houba-Herlin N., Hara H., Inouye M., Hirota Y.;
"Binding of penicillin to thiol-penicillin-binding protein 3 of *Escherichia coli*: identification of its active site.";
Mol. Gen. Genet. 201:499-504(1985).

[10] PROCESSING.

MEDLINE=90036670; **PubMed**=2681146; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Nagasawa H., Sakagami Y., Suzuki A., Suzuki H., Hara H., Hirota Y.;
"Determination of the cleavage site involved in C-terminal processing of penicillin-binding protein 3 of *Escherichia coli*.";

J. Bacteriol. 171:5890-5893(1989).

[11] MUTANT PBPBR1.

MEDLINE=89008105; PubMed=3049550; [NCBI, ExPASy, EBI, Israel, Japan]

Taschner P.E., Ypenburg N., Spratt B.G., Woldringh C.L.;

"An amino acid substitution in penicillin-binding protein 3 creates pointed polar caps in Escherichia coli.";

J. Bacteriol. 170:4828-4837(1988).

[12] TOPOLOGY.

MEDLINE=90014188; PubMed=2677607; [NCBI, ExPASy, EBI, Israel, Japan]

Bowler L.D., Spratt B.G.;

"Membrane topology of penicillin-binding protein 3 of Escherichia coli.";

Mol. Microbiol. 3:1277-1286(1989).

Comments

- **FUNCTION:** CELL WALL FORMATION. ESSENTIAL FOR THE FORMATION OF A SEPTUM OF THE MUREIN SACCULUS. SYNTHESIS OF CROSS-LINKED PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES.
- **PATHWAY:** FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
- **SUBCELLULAR LOCATION:** INNER MEMBRANE. THE BULK OF THE MOLECULE, EXCEPT FOR THE N-TERMINAL MEMBRANE ANCHOR REGION, PROTRUDES INTO THE PERIPLASMIC SPACE, WHERE IT ACTS ON MUREIN.
- **DOMAIN:** HAS AN N-TERMINAL PENICILLIN INSENSITIVE TRANSGLYCOSYLASE DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) & A CARBOXY-TERMINAL PENICILLIN-SENSITIVE TRANSPEPTIDASE DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNITS).
- **MISCELLANEOUS:** MUTANT PBPBR1 WHICH WAS OBTAINED AFTER SELECTION FOR INCREASED RESISTANCE TO CEPHALEXIN, CAUSES A CHANGE IN THE SHAPE OF THE CELL: THE POLAR CAPS ARE POINTED.
- **SIMILARITY:** BELONGS TO THE TRANSPEPTIDASE FAMILY.

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Cross-references

EMBL	K00137; AAA24300.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	X55034; CAA38861.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	D10483; BAB96652.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE000118; AAC73195.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE005185; AAG54388.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AP002550; BAB33511.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	S49802; AAB24312.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	S49875; AAB24310.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	X55814; CAA39333.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	A03419; ZPECP3.
	B45278; B45278.
MEROPS	S40594; S40594.
	S12.UNW; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
EcoGene	EG10341; ftsI.
EcoCyc	EG10341; ftsI.

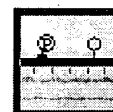
CMR	P04286 ; B0084.
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InterPro	IPR001460 ; Transpeptidase.
	Graphical view of domain structure.
Pfam	PF00905 ; Transpeptidase; 1.
	PF03717 ; PBP_dimer; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	P04286 .
ProtoNet	P04286 .
ProtoMap	P04286 .
PRESAGE	P04286 .
DIP	P04286 .
ModBase	P04286 .
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Inner membrane; Peptidoglycan synthesis; Cell division; Cell wall; Antibiotic resistance; Multifunctional enzyme; Cell shape; Transmembrane; Complete proteome.

Features

Key	From	To	Length	Description
CHAIN	1	577	577	PEPTIDOGLYCAN SYNTHETASE FTSI.
PROPEP	578	588	11	
DOMAIN	1	18	18	CYTOPLASMIC (<i>POTENTIAL</i>).
TRANSMEM	19	39	21	<i>POTENTIAL</i> .
DOMAIN	40	577	538	PERIPLASMIC (<i>POTENTIAL</i>).
ACT_SITE	307	307		ACYLATED BY PENICILLIN.
VARIANT	361	361		N -> S (IN MUTANT PBPBR1).
MUTAGEN	307	307		S->A,T: UNABLE TO BIND PENICILLIN.
MUTAGEN	307	307		S->C: STILL ABLE TO BIND PENICILLIN.


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Sequence information

Length: **588 AA** [This is the length of the unprocessed precursor]

Molecular weight: **63877 Da** [This is the MW of the unprocessed precursor]

CRC64: **C89A403D5980B2CD** [This is a checksum on the sequence]

10	20	30	40	50	60
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70	80	90	100	110	120
SLRVQQVSTS	RGMITDRSGR	PLAVSVPVKA	IWADPKEVHD	AGGISVGDRW	KALANALNIP
130	140	150	160	170	180
LDQLSARINA	NPKGRFIYLA	RQVNPDMADY	IKKLKLPGIH	LRRESRRYYP	SGEVTAGHLIG
190	200	210	220	230	240
FTNVDSQGIE	GVEKSFDKWL	TGQPGERIVR	KDRYGRVIED	ISSTDSQAAH	NLALSIDERL


```

      250      260      270      280      290      300
      |      |      |      |      |      |
QALVYRELNN AVAFNKAESG SAVLVDVNTG EVLAMANSPTS YNPNNLSGTP KEAMRNRTIT

      310      320      330      340      350      360
      |      |      |      |      |      |
DVFEPGSTVK PMVVM TALQR GVVRENSVLN TIPYRINGHE IKDVARYSEL TLTGVLQKSS

      370      380      390      400      410      420
      |      |      |      |      |      |
NVGVSKLALA MPSSALVDTY SRFGLGKATN LGLVGERSGL YPQQRWSDI ERATFSFGYG

      430      440      450      460      470      480
      |      |      |      |      |      |
LMVTPLQLAR VYATIGSYGI YRPLSITKVD PPVPGERVFP ESIVRTVVHM MESVALPGGG

      490      500      510      520      530      540
      |      |      |      |      |      |
GVKAAIKGYR IAIKTGTAKK VGPDGRYINK YIAYTAGVAP ASQPRFALVV VINDPQAGKY

      550      560      570      580
      |      |      |      |
YGGAVSAPVF GAIMGGVLR T MNIEPDALT GDKNFVINQ GEGTGGRS

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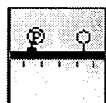
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Tools Sequence analysis tools: [ProtParam](#), [ProtScale](#),
[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
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